AMENDMENTS TO THE SPECIFICATION

The following replacements to the Specification are requested, with deletions indicated by strikethroughs and insertions indicated by underlining.

Please replace the Abstract with the following text:

A chimeric LL2 monoclonal antibody (mAb) is described in which the complementarity determining regions (CDRs) ~~of the light and heavy chains~~ of the murine LL2 ~~anti-B-lymphoma, anti-leukemia cell monoclonal antibody~~ mAb ~~has been~~ are recombinantly joined to the human ~~kappa and IgG.sub.~~1 constant region domains~~, respectively~~, which retains the immunospecificity and B-cell lymphoma and leukemia cell internalization capacity of the ~~parental~~ murine LL2 ~~monoclonal antibody~~ (mAB), and which ~~has the potential of exhibiting~~ exhibits reduced human anti-mouse antibody production activity (HAMA). A humanized LL2 ~~monoclonal antibody~~ mAb is described in which the CDRs ~~of the light and heavy chains have been~~ are recombinantly joined to a framework sequence of human ~~light and heavy chains~~ variable regions, ~~respectively,~~ and subsequently linked to human ~~kappa and IgG.sub.1~~ constant region domains, ~~respectively,~~ which retains the immunospecificity and B-lymphoma and leukemia cell internalization capacities of the ~~parental~~ murine and chimeric LL2 ~~monoclonal antibodies~~ mABs, and ~~which~~ has the potential for exhibiting reduced ~~human anti-mouse antibody production activity~~ HAMA. ~~Vectors for producing recombinant chimeric and humanized chimeric monoclonal antibody mAbs are provided~~. Isolated DNAs encoding ~~the amino acid sequences of~~ the LL2 variable ~~light~~ and ~~heavy chain and~~ CDR framework regions are described. Conjugates of chimeric and humanized chimeric LL2 antibodies with cytotoxic agents or labels find use in therapy and diagnosis of B-cell lymphomas and leukemias.

Please replace paragraph [0040] with the following text:

[0040] As the VK-appended carbohydrate moiety of the cLL2 mAb is shown herein not to be involved in binding to B-lymphoma cells, it is preferred to use conjugates in which the reagent is bound to the antibody through such carbohydrate moieties, such as through oxidized carbohydrate derivatives. Methods for the production of such conjugates and their use in diagnostics and therapeutics are provided, for example. in Shih et al., U.S. Pat. No. 5,057,313,

Shih et al., Int. J. Cancer 41: 832 (1988), and copending, commonly owned Hansen et al., U.S. Ser. No. 08/162,912, U.S. Pat. No. [[*]]5,443,953, the contents of which are incorporated herein by reference. Direct linkage of the reagent to oxidized carbohydrate without the use of a polymeric carrier is described in McKearn et al., U.S. Pat. No. 5,156,840, which is also incorporated by reference.

Please replace paragraph [0043] with the following text:

[0043] An important aspect of this invention is that antibody variable domains can be modeled by computer modeling (see, for example, Dion, in Goldenberg et al. eds., Cancer Therapy With Radiolabeled Antibodies, CRC Press, Boca Raton, Fla., 1994), which is incorporated by reference. In general, the 3-D structure for both the mLL22 and hLL2 mAbs are best modeled by homology. The high frequency of residue identities (75.0 to 92.3%) between the deduced primary sequences of mLL2 light chain FR regions and human REI (VK) facilitates this approach because of the availability of crystallographic data from the Protein Data Bank (PDR Code 1 REI, Bernstein et al., J. Mol. Biol. 112: 535 (1977)), which is incorporated by reference. Similarly, antibody EU (VH) sequences can be selected as the computer counterparts for FR1 to FR3 of the mLL2 heavy chain; FR4 was based on NEWM. As X-ray coordinate data is currently lacking for the EU sequence, NEWM structural data (PDR Code 3FAB) for FRs 1 to 4 can be used, and amino acid side groups can be replaced to correspond to mLL2 or EU (hLL2) as needed. The CDR of the light chain can be modeled from the corresponding sequence of 1MCP (L1 and L2) and 1REI (L3). For heavy chain CDRs, H1 and H2 can be based on 2HFL and 1MCP, respectively, while H3 can be modeled de novo. Wherever possible, side group replacements should be performed so as to maintain the torsion angle between Cα and C.β. Energy minimization may be accomplished by the AMBER forcefield (Weiner et al, *J. Amer. Chem. Soc.* 106: 765 (1984) using the convergent method. Potentially critical FR-CDR interactions can be determined by initially modeling the light and heavy variable chains of mLL2. All FR residues within a 4.5 Å radius of all atoms within each CDR can thereby be identified and retained in the final design model of hLL2.